Manuals+ — User Manuals Simplified.

Apps iMed Web Application User Manual

iMed User Manual

Contents

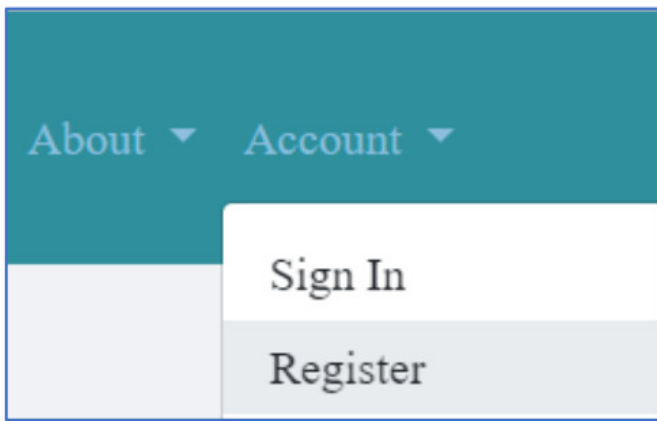## Introduction

1.1. Purpose
The purpose of this web application is to take raw information and allow manipulating it in a manner that gives results useful in decision making. This can be to train a model with raw data or predicting the outcome using models and analysis.

1.2. Navigational Menu
The navigational menu on the top of the page holds all the links to get to where you need to be. If you ever get lost, you can always click the back arrow to get to a familiar page, go back home, or find the page you are looking for within the navigational menu.

1.3. Account
If you don't already have an account, you must register to use the application. To do so, click the account button on the top right and click register. Then enter your username, password, and email to proceed.
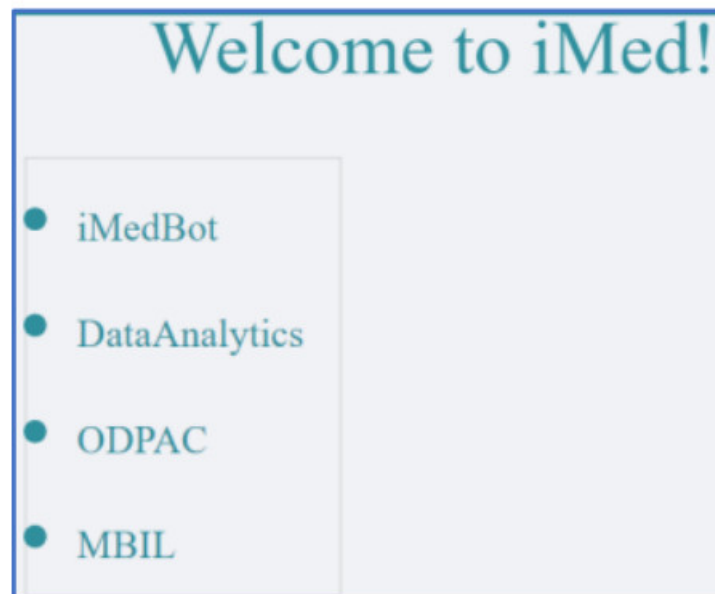
If you already have an account, sign in with your username and password.


Home Page

By clicking on the items on the left of the page, a description of each will appear in the middle of the page to help you understand what each one does.

iMedBot

The iMedBot application presents an interface that fosters easy user interaction with agents, enabling personalized prediction and model training. It serves as the first step towards transforming the outcomes of deep

learning research into an online tool, which has the potential to spark additional research pursuits in this domain. Its respective user manual can be found here.
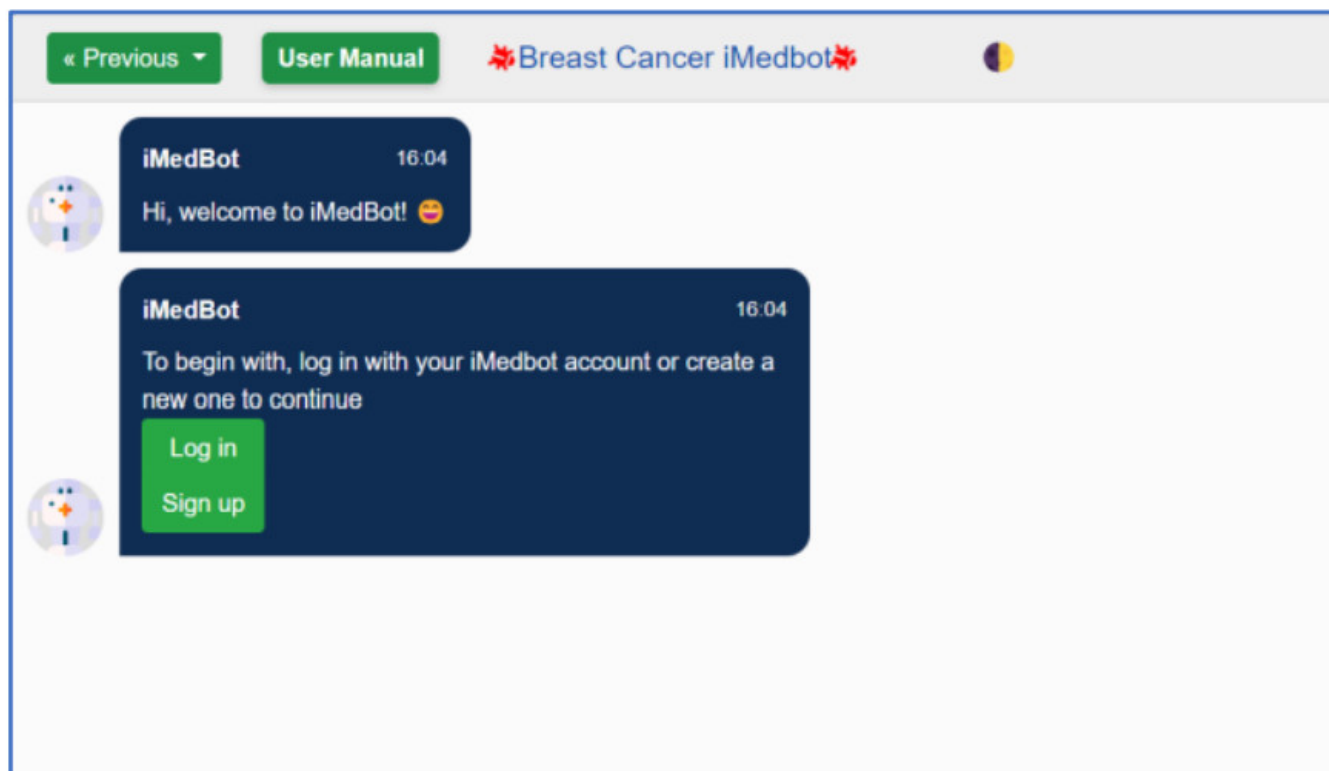
Data Analysis

4.1. Retrieve Subsets
This section lets the user edit their dataset. You can choose to either upload a new dataset or use an existing one from the drop-down menu.

Once the dataset has been uploaded, you can choose what action you would like to take by clicking one of the options on the left side menu.

4.1.1. Retrieve Subsets Based on Filters
This section allows getting a smaller subset of the original dataset based on given filters. Choose the values that you want in the subset and then choose the columns that you want shown in the final dataset.

4.1.2. Return Sorted Results

This returns the dataset in a sorted form. Choose the target column, sorting order, number of rows to return, and which columns to show in the final output.

4.1.3. Expand the Dataset

This allows the user to expand a singular column stored as a dictionary into an actual table that the user can then manipulate. It takes a nested dataset and moves what is required by the user into the top-most layer. First, upload a dataset that includes a column with a nested dataset. If a column that needs expanding is automatically detected, choose which column to expand and which columns to extract from the nested information. Click submit and you can view your information as columns of a table instead of nested data.

4.2. Merge Files

By selecting and uploading multiple datasets by ctrl clicking (command for mac), this will merge them into one larger dataset than be used for something else.

Upload Datasets: ❓

Choose Files No file chosen

Does this file include header? ❓ Yes ▾

Please choose the delimiter for this dataset ❓ Comma - "," ▾

Upload

Just select all datasets and fill in the required information. This will save the new dataset to the iMed application and is then available for download.

4.3. Plot Functions

This section lets the user plot their dataset. Choose one of the options on the left-hand side menu and then fill in the required fields to obtain your plot. Below are the types of plots you can make from your data:

- Plot ROC Curves
- Box Plot
- Trend Analysis
- 3D Scatter
- Heatmap Plot

4.4. Statistical Analysis

This section lets us run statistical tests on our dataset. Choose a test to run from the left side menu and fill in the fields to run the tests. Below are the types of tests that are available:

- wilcoxon sign-ranked test
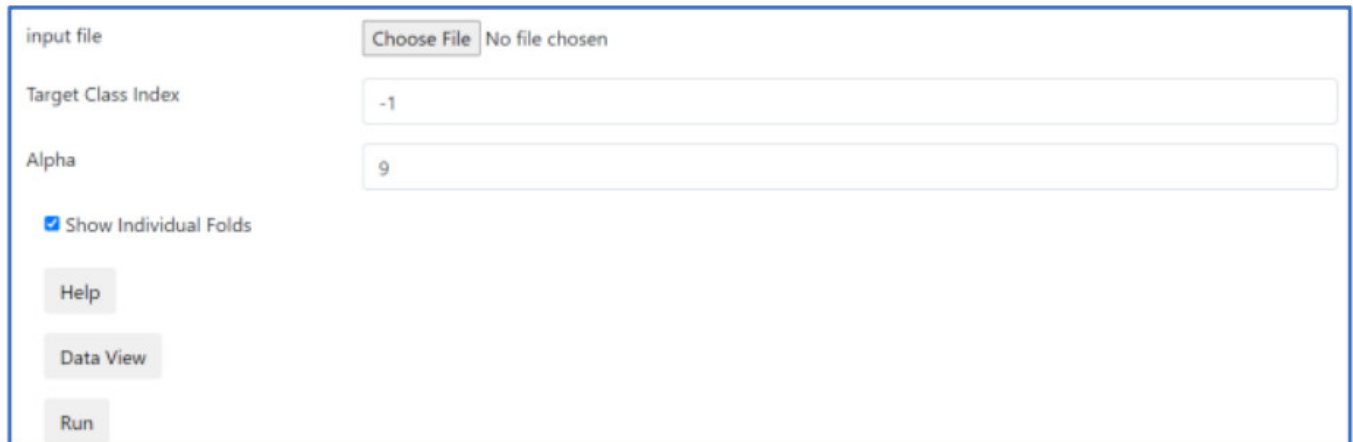- chi-squared test
- feature importance

ODPAC

5.1. Learn

This page includes a brief description of each type of resource available on this page. Clicking the button at the top of each section will link to another page allowing the user to use or learn more about the topic.

5.1.1. Epistasis

This page lets us use MBS, a search algorithm to learn from data. Specifically, it allows us to study epistasis, the interaction between two or more genes that affect the phenotype. This is useful to profile diseases in the genetic aspect. Conventional methods are not suited to handle the high-dimensional data found in genome-wide association studies (GWAS). The Multiple Beam Search (MBS) algorithm allows detecting interacting genes at a much faster rate. Upload the data that you want to use and then input the required fields. For more in-depth information, find the full paper here.
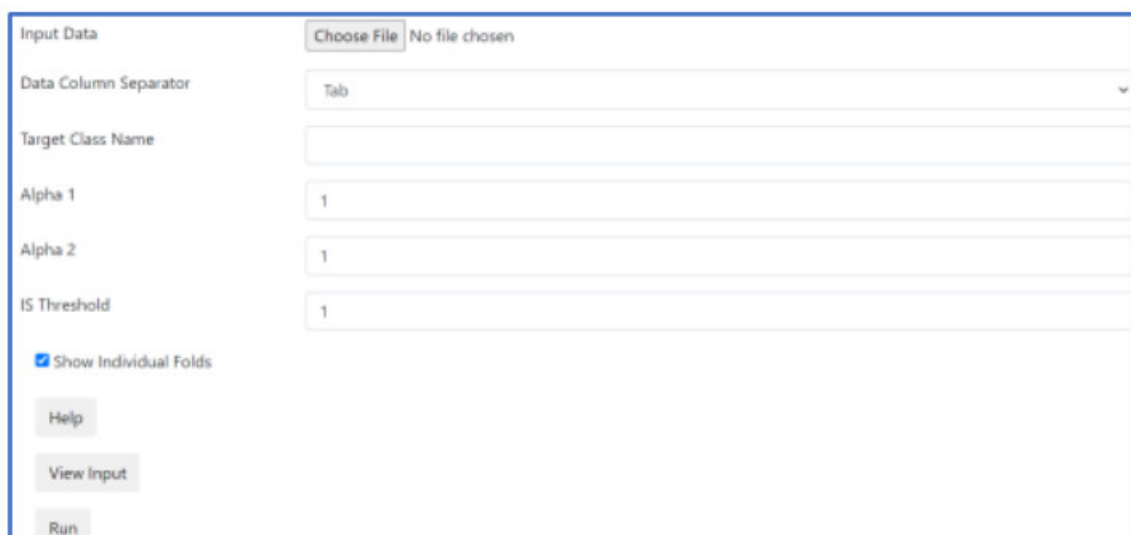

5.1.2. Risk Factors

This page lets us use the IGain package to learn interactions between data. It specifically learns interactions from high-dimensional data using a heuristic search. This method builds on the Exhaustive_IGain method previously developed to learn interactions from low-dimensional data. Upload the data and then input the required fields. More information about the IS thresholds and iGain can be found here.

5.1.3. Prediction Models

This section allows the use of prediction models already pre-built on top of machine learning models to expedite its use. This allows their use without the use of coding and prior experience to predict models using their own dataset. There a numerous prediction models available to the user including Logistic, Regression, Support Vector Machines (SVMs), Decision Trees, and many more. The full list of prediction methods are found on the right side of the page here.

5.2. Prediction

This section allows predictions from a shared model previously uploaded. First upload a shared model if not done so already. Then choose the model to use for prediction by clicking the model name. Then upload the data for the prediction model to use. This can be done either manually using the form at the bottom of the page or using the template available for download. If using the template, upload the dataset file and click submit to receive the model prediction.

5.3. Decision Support

Decision support provides classification and can guide treatment choices from information supplied to the system. It has been trained from data to recommend the optimal treatment procedure based on a patient's features. More information regarding Clinical Decision Support Systems (CDSS) can be found here.

The System Recommendation takes a patient's features and recommends treatment procedure and predicts the future probability of 5 year metastasis. The User Intervention takes both the patient features and the treatment procedure to predict the future probability of 5 year metastasis based on current treatment instead of optimal treatment.

MBIL

The Markov Blanket and Interactive Risk Factor Learner (MBIL) is an algorithm that learns single and interactive risk factors that have a direct influence on a patient's outcome. Click "go to MBIL" to be redirected to the Python Package Index (PyPI) for the MBIL package located here. More information about MBIL can be found at BMC Bioinformatics.

Datasets

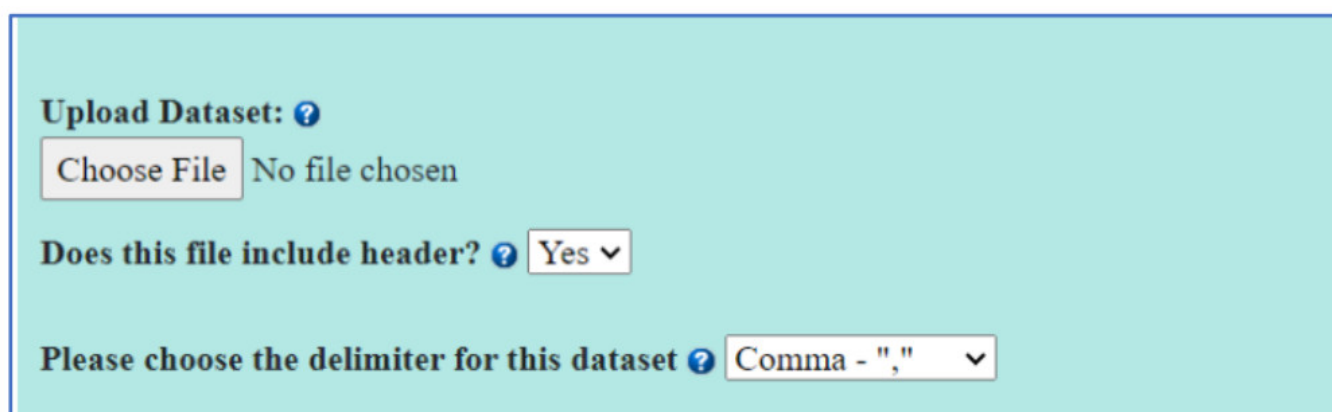This section allows the user to see and upload new datasets to the web application.

7.1. See All Datasets Available

To see all datasets available, simply click "Show Available Datasets."
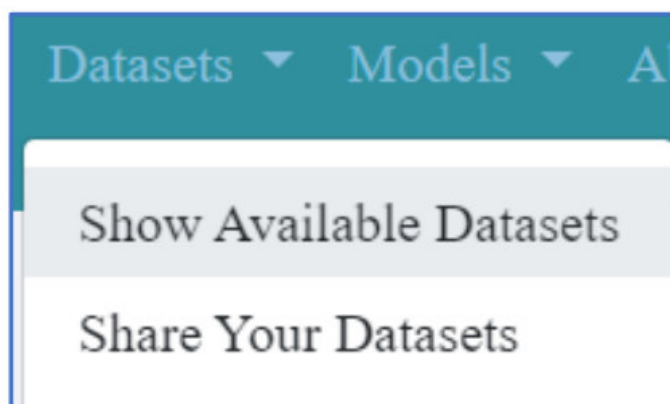
7.2. Upload a Dataset

To upload a dataset, click "Share Your Datasets" and then fill in required information as stated on the webpage. First, upload the dataset and fill in required fields.

Then, fill in the fields below or upload a text file with the information filled in. An example of how to organize the information so the application can understand it is given below.
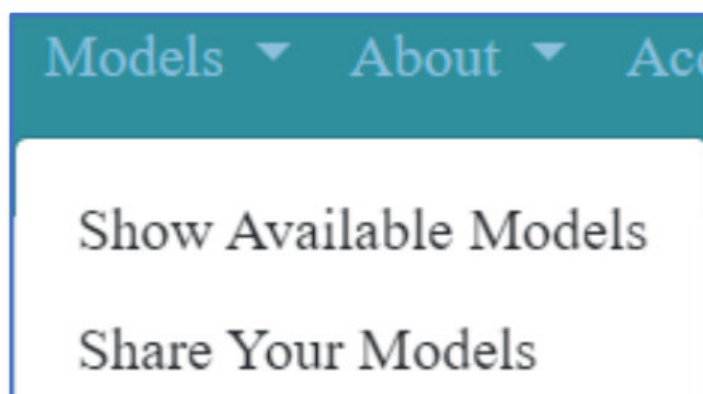
```
provider: <your full name as a submitter>
curator: <the name of the person who generated the dataset>
original_publication: <the citation/reference to the original paper or the link to the paper>
restriction: <Your restriction for other users to use your model>
```

Models

This section allows the user to see models available to them and share a model.

8.1. See All Models Available

To see all models available, click "Show Available Models."

8.2. Share a Model

To share a model, click on "Share Your Models" and then upload a model file trained by tensor flow or PyTorch.

8.2.1. Related Dataset

You should then upload the related dataset which includes the headers. The class/label for the dataset should be in the last column.

8.2.2. Predictors and Class information

If the dataset includes all the features, the feature form can be skipped after uploading the dataset. However, if they are not all included, this information must be provided in the description file or within the feature form. Choose the option from the drop down indicating how you intend to provide the predictors and class information.

If using the description option, you can either fill in the fields or upload a text file with the information filled in. An example of how to organize the information is given below.

```
provider: <your full name as a submitter>
curator: <the name of the person who generated the model>
restriction: <Your restriction for a user to use your model>
method: <the machine learning method that is being used to generate the model>
hyperparametersetting: <the hyperparametersettings to train your model>
predictors: <{'discrete_predictor1':[[1,2,3],'discrete'], 'continuous_predictor1':[[2-3],'continuous']}>
class: <{'class_name': [[0, 1], 'discrete']}>
```

Documents / Resources

Apps iMed Web Application [pdf] User Manual
iMed, iMed Web Application, Web Application